SEQUENCE LISTING

<110> Lassner, M
Post-Beittenmiller, D
Savidge, B
Weiss, J

<120> Nucleic Acid Sequences Involved in
Tocopherol Synthesis

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<150> 60/129,899
<151> 1999-04-15

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<151> 1999-07-30

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Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu
50 55 60
Tyr Pro Lys His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln
65 70 75 80
Pro Glu Ala Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser
85 90 95
Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr
100 105 110
Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Val Glu Lys Val Ser
115 120 125
Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala
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Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp
145 150 155 160
Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
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Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
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Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp

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Leu Ala Val Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile
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Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile
            260                 265                 270
Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe
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Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser
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305                 310                 315                 320
Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser
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Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
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Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys
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50 55 60
Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
65 70 75 80
Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
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Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys
100 105 110
Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
115 120 125
Lys Leu Ala Arg Leu Asp Lys Pro Ile Gly Thr Trp Leu Leu Ala Trp
130 135 140
Pro Cys Met Trp Ser Ile Ala Leu Ala Ala Asp Pro Gly Ser Leu Pro
145 150 155 160
Ser Phe Lys Tyr Met Ala Leu Phe Gly Cys Gly Ala Leu Leu Leu Arg
165 170 175

Gly Ala Gly Cys Thr Ile Asn Asp Leu Leu Asp Gln Asp Ile Asp Thr
180 185 190
Lys Val Asp Arg Thr Lys Leu Arg Pro Ile Ala Ser Gly Leu Leu Thr
195 200 205
Pro Phe Gln Gly Ile Gly Phe Leu Gly Leu Gln Leu Leu Leu Gly Leu
210 215 220
Gly Ile Leu Leu Gln Leu Asn Asn Tyr Ser Arg Val Leu Gly Ala Ser
225 230 235 240
Ser Leu Leu Leu Val Phe Ser Tyr Pro Leu Met Lys Arg Phe Thr Phe
245 250 255
Trp Pro Gln Ala Phe Leu Gly Leu Thr Ile Asn Trp Gly Ala Leu Leu
260 265 270
Gly Trp Thr Ala Val Lys Gly Ser Ile Ala Pro Ser Ile Val Leu Pro
275 280 285
Leu Tyr Leu Ser Gly Val Cys Trp Thr Leu Val Tyr Asp Thr Ile Tyr
290 295 300
Ala His Gln Asp Lys Glu Asp Asp Val Lys Val Gly Val Lys Ser Thr
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Ala Leu Arg Phe Gly Asp Asn Thr Lys Leu Trp Leu Thr Gly Phe Gly
325 330 335
Thr Ala Ser Ile Gly Phe Leu Ala Leu Ser Gly Phe Ser Ala Asp Leu
340 345 350
Gly Trp Gln Tyr Tyr Ala Ser Leu Ala Ala Ala Ser Gly Gln Leu Gly
355 360 365
Trp Gln Ile Gly Thr Ala Asp Leu Ser Ser Gly Ala Asp Cys Ser Arg
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Ala Lys Leu Gly Ile Thr Gly Val Arg Ser Asp Ala Asn Arg Val Phe
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Ala Thr Ala Thr Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Glu Ile
65                  70                  75                  80
Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg
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Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala
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Thr Ser Gly Thr Gly Tyr Ile Leu Gly Thr Gly Asn Ala Ala Ile Ser
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165 170 175
Pro His Ala Val Ala Trp Ala Thr Ile Ala Gly Ala Ser Gly Ala Cys
180 185 190
Leu Leu Ala Ser Lys Thr Asn Met Leu Ala Ala Gly Leu Ala Ser Ala
195 200 205
Asn Leu Val Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Gln Leu His
210 215 220
Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu
225 230 235 240
Leu Gly Trp Ala Ala Ala Ser Gly Gln Ile Ser Tyr Asn Ser Met Ile
245 250 255
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260 265 270
Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu
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Ser Leu Phe Asp Pro Ser Gly Lys Arg Ile Ala Ala Val Ala Leu Arg
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Asn Cys Phe Tyr Met Ile Pro Leu Gly Phe Ile Ala Tyr Asp Trp Gly
305 310 315 320
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325 330 335
Ile Ala Ala Thr Ala Phe Ser Phe Tyr Arg Asp Arg Thr Met His Lys
340 345 350
Ala Arg Lys Met Phe His Ala Ser Leu Leu Phe Leu Pro Val Phe Met
355 360 365
Ser Gly Leu Leu Leu His Arg Val Ser Asn Asp Asn Gln Gln Gln Leu
370 375 380
Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr
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35 40 45
Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
50 55 60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
85 90 95
Val Val Met Gly Asn Lys Val Val Ala Leu Leu Ala Thr Ala Val Glu
100 105 110
His Leu Val Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln
115 120 125
Arg Tyr Ser Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala
130 135 140
Ser Leu Ile Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln
145 150 155 160
Thr Ala Glu Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly
165 170 175
Leu Ala Phe Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser
180 185 190
Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile
195 200 205
Thr Ala Pro Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu
210 215 220
Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu
225 230 235 240
Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala
245 250 255
Met Glu His Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu
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Thr Asp Asn Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu
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35 40 45
Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
50 55 60
Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80
Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
85 90 95
Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp Phe Leu Leu
100 105 110
Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr Glu Val Val
115 120 125
Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly Glu Thr Met
130 135 140
Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp Tyr Tyr Met
145 150 155 160
Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys
165 170 175
Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala Val Leu Ala
180 185 190
Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp
195 200 205
Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu
210 215 220
Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met
225 230 235 240
Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp
245 250 255
Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly
260 265 270
Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala
275 280 285
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tagtggctgc gagcaccaaa ggagctgcca ttttcagcag agttgagcct gatgtgacag 480
aacaaatgta cgagtttggg aagaatctcg gtctctcttt ccagatagtt gatgatattt 540
tggatttcac tcagtcgaca gagcagctcg ggaagccagc agggagtgat ttggctaaag 600
gtaacttaac agcacctgtg attttcgctc tggagaggga gccaaggcta agagagatca 660

ttgagtcaaa gttctgtgag gcgggttctc tggaagaagc gattgaagcg gtgacaaaag 720
gtgggggat taagagagca c 741

<210> 15
<211> 1087
<212> DNA
<213> Arabidopsis sp

<400> 15
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cctctgg 1087

<210> 16
<211> 1164
<212> DNA
<213> Arabidopsis sp

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gctgcttcag ggaactttca ttggacccca gaggatgttg ctaagtcgat tctttgcatg 420
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gatatcgacg caattaatga gccatatcgt ccaattccat ctggagcaat atcagagcca 540
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gatgtgtggg cagggcatac cactcccact gtcttctatc ttgctttggg aggatcattg 660
ctatcttata tatactctgc tccacctctt aagctaaaac aaaatggatg ggttggaaat 720
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cagctttctg ttgccggata tctattagca tctgggaaac cttattatgc gttggcgttg 1020
gttgctttga tcattcctca gattgtgttc cagtttaaat actttctcaa ggaccctgtc 1080
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<210> 17
<211> 387
<212> PRT
<213> Arabidopsis sp

<400> 17

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Val	Glu	Phe	Thr	Arg	Arg	Arg	Ser	Gly	Phe	Ser	Thr	Leu	Ile	Tyr	Glu
		35					40					45			
Ser	Pro	Gly	Arg	Arg	Phe	Val	Val	Arg	Ala	Ala	Glu	Thr	Asp	Thr	Asp
	50					55					60				
Lys	Val	Lys	Ser	Gln	Thr	Pro	Asp	Lys	Ala	Pro	Ala	Gly	Gly	Ser	Ser
65					70					75					80
Ile	Asn	Gln	Leu	Leu	Gly	Ile	Lys	Gly	Ala	Ser	Gln	Glu	Thr	Asn	Lys
				85					90					95	
Trp	Lys	Ile	Arg	Leu	Gln	Leu	Thr	Lys	Pro	Val	Thr	Trp	Pro	Pro	Leu
			100					105					110		
Val	Trp	Gly	Val	Val	Cys	Gly	Ala	Ala	Ala	Ser	Gly	Asn	Phe	His	Trp
		115					120					125			
Thr	Pro	Glu	Asp	Val	Ala	Lys	Ser	Ile	Leu	Cys	Met	Met	Met	Ser	Gly
	130					135					140				
Pro	Cys	Leu	Thr	Gly	Tyr	Thr	Gln	Thr	Ile	Asn	Asp	Trp	Tyr	Asp	Arg
145					150					155					160

Asp Ile Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala
165 170 175
Ile Ser Glu Pro Glu Val Ile Thr Gln Val Trp Val Leu Leu Leu Gly
180 185 190
Gly Leu Gly Ile Ala Gly Ile Leu Asp Val Trp Ala Gly His Thr Thr
195 200 205
Pro Thr Val Phe Tyr Leu Ala Leu Gly Gly Ser Leu Leu Ser Tyr Ile
210 215 220
Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn
225 230 235 240
Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln
245 250 255
Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu
260 265 270
Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser
275 280 285
Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe
290 295 300
Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr
305 310 315 320
Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr
325 330 335
Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe
340 345 350
Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala
355 360 365
Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala
370 375 380
Ser Gln His
385

<210> 18
<211> 981
<212> DNA
<213> Arabidopsis sp

<400> 18
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gggtcgttga acttcgatct gaggacgtat tggacgactc tgatcaccga gatcaaccag 180
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tctgtactcg cacaaggcgc caagcgtgcc cctcctgtga tgtgtgtggc ggcctgcgag 300
ctcttcggtg gcgatcgcct cgccgctttc cccaccgcct gtgccctaga aatggtgcac 360
gcggcttcgt tgatacacga cgacctcccc tgtatggacg acgatcctgt gcgcagagga 420
aagccatcta accacactgt ctacggctct ggcatggcca ttctcgccgg tgacgccctc 480
ttcccactcg ccttccagca cattgtctcc cacacgcctc ctgaccttgt tccccgagcc 540
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ttcggagcca tgggtgaatg ctctgccgtg tgcggtggcc tattgggcgg tgccactgag 720
gatgagctcc agagtctccg aaggtacggg agagccgtcg ggatgctgta tcaggtggtc 780
gatgacatca ccgaggacaa gaagaagagc tatgatggtg gagcagagaa gggaatgatg 840
gaaatggcgg aagagctcaa ggagaaggcg aagaaggagc ttcaagtgtt tgacaacaag 900
tatggaggag gagacacact tgttcctctc tacaccttcg ttgactacgc tgctcatcga 960
cattttcttc ttcccctctg a 981

<210> 19
<211> 245
<212> DNA
<213> GLycine sp

<400> 19
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tcttgcactt gcttgggtac catgatggtt gctgcatctg ctaactcttt gaatcaggtg 120
tttgagatca ataatgatgc taaaatgaag agaacaagtc gcaggccact accctcagga 180
cgcatcacaa tacctcatgc agttggctgg gcatcctctg ttggattagc tggtacggct 240
ctact 245

<210> 20
<211> 253
<212> DNA
<213> Glycine sp

<400> 20
attggctttc caagatcatt gggttttctt gttgcattca tgaccttcta ctccttgggt 60
ttggcattgt ccaaggatat acctgacgtt gaaggagata aagagcacgg cattgattct 120
tttgcagtac gtctaggtca gaaacgggca ttttggattt gcgtttcctt ttttgaaatg 180
gctttcggag ttggtatcct ggccggagca tcatgctcac acttttggac taaaattttc 240
acgggtatgg gaa 253

<210> 21
<211> 275
<212> DNA

<213> Glycine sp

<400> 21
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aagcatacgg catcgatact ttagcgatac gtttgggtca aaaatgggta ttttggattt 120
gcattatcct ttttgaaatg gcttttggag ttgccctctt ggcaggagca acatcttctt 180
acctttggat taaaattgtc acgggtctgg gacatgctat tcttgcttca attctcttgt 240
accaagccaa atctatatac ttgagcaaca aagtt 275

<210> 22
<211> 299
<212> DNA
<213> Glycine sp

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 22
ccanaatang tncatcttng aaagacaatt ggcctcttca acacacaagt ctgcatgtga 60
agaagaggcc aattgtcttt ccaagatcac ttatngtggc tattgtaatc atgaacttct 120
tctttgtggg tatggcattg gcaaaggata tacctanctg ttgaaggaga taaaatatat 180
ggcattgata cttttgcaat acgtataggt caaaaacaag tattttggat ttgtattttc 240
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<210> 23
<211> 767
<212> DNA
<213> Glycine sp

<400> 23
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tctgatgttg aaatagacaa gataaacaag ccgtatcttc cattagcatc tggggaatat 120
tcctttgaaa ctggtgtcac tattgttgca tctttttcaa ttctgagttt ttggcttggc 180
tgggttgtag gttcatggcc attattttgg gccctttttg taagctttgt gctaggaact 240
gcttattcaa tcaatgtgcc tctgttgaga tggaagaggt ttgcagtgct tgcagcgatg 300
tgcattctag ctgttcgggc agtaatagtt caacttgcat ttttccttca catgcagact 360
catgtgtaca agaggccacc tgtcttttca agaccattga tttttgctac tgcattcatg 420
agcttcttct ctgtagttat agcactgttt aaggatatac ctgacattga aggagataaa 480
gtatttggca tccaatcttt ttcagtgtgt ttaggtcaga agccggtgtt ctggacttgt 540

gttacccttc ttgaaatagc ttatggagtc gccctcctgg tgggagctgc atctccttgt 600
ctttggagca aaattttcac gggtctggga cacgctgtgc tggcttcaat tctctggttt 660
catgccaaat ctgtagattt gaaaagcaaa gcttcgataa catccttcta tatgtttatt 720
tggaagctat tttatgcaga atacttactc attccttttg ttagatg 767

<210> 24
<211> 255
<212> PRT
<213> Glycine sp

<400> 24

Val Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly
1 5 10 15
Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr
20 25 30
Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile
35 40 45
Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly
50 55 60
Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr
65 70 75 80
Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val
85 90 95
Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
100 105 110
Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val
115 120 125
Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser
130 135 140
Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys
145 150 155 160
Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val
165 170 175
Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu
180 185 190
Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly
195 200 205
Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser
210 215 220
Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile
225 230 235 240

Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
245 250 255

<210> 25
<211> 360
<212> DNA
<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(360)
<223> n = A,T,C or G

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tcaggcttat cttggcctga cattcaactg gggagcttta ctagggtggg ctgctattaa 120
ggaaagcata gaccctgcaa atcatccttc cattgtatac agctggtatt tgttggacgc 180
tggtgtatga tactatatat gcgcatcagg tgtttcgcta tccctacttt catattaatc 240
cttgatgaag tggccatttc atgttgtcgc ggtggtctta tacttgcata tctccatgca 300
tctcaggaca aagangatga cctgaaagta ggagtccaag tccacagctt aagatttggg 360

<210> 26
<211> 299
<212> DNA
<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 26
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aatgaaaagg acaatgcgtg ccccctgcca tctggtcgca ttagtcctgc acatgctgcg 120
atgtgggcta caagtgttgg agttgcagga acagctttgt tggcctggaa ggctaatggc 180
ttggcagctg ggcttgcagc ttctaatctt gttctgtatg catttgtgta tacgccgttg 240
aagcaaatac accctgttaa tacatgggtt ggggcagtcg ttggtgccat cccaccact 299

<210> 27
<211> 255
<212> DNA

<213> Zea sp

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

<400> 27
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tgcttcggca gcttagcact cagtggttac aatgctgacc ttggttggtg tttagtgtga 180
tgcttgagcg aagaatggta tngtttttac ttgatattga ctccagacct gaaatcatgt 240
tggacagggt ggccc 255

<210> 28
<211> 257
<212> DNA
<213> Zea sp

<400> 28
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gcaaaatgga tttgtgttgg agcaattgat atcactcaat tatctgttgc aggttaccta 120
ttgagcaccg gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcaggtg 180
ttctttcagt tccagtactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggca 240
agcgcacaac cattctt 257

<210> 29
<211> 368
<212> DNA
<213> Zea sp

<400> 29
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aagaaggtct tttggatctg cgttggcttg cttgagatgg cctacagcgt tgcgatactg 180
atgggagcta cctcttcctg tttgtggagc aaaacagcaa ccatcgctgg ccattccata 240
cttgccgcga tcctatggag ctgcgcgcga tcggtggact tgacgagcaa agccgcaata 300
acgtccttct acatgttcat ctggaagctg ttctacgcgg agtacctgct catccctctg 360
gtgcggtg 368

<210> 30

<211> 122
<212> PRT
<213> Zea sp

<400> 30
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Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg
20 25 30
Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val
35 40 45
Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr
50 55 60
Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile
65 70 75 80
Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser Val Asp Leu Thr Ser
85 90 95
Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr
100 105 110
Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg
115 120

<210> 31
<211> 278
<212> DNA
<213> Zea sp

<400> 31
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gcgagttaca tcagcttgcc ctggtgggct ggccaggcgt tatttggaac tcttacacca 120
gatatcattg tcttgactac tttgtacagc atagctgggc tagggattgc tattgtaaat 180
gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tgttgctttt 240
gggatggaaa ctgcaaaatg gatttgtgtt ggagcaat 278

<210> 32
<211> 292
<212> PRT
<213> Synechocystis sp

<400> 32
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Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile
            20                  25                  30
Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu
        35                  40                  45
Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu
    50                  55                  60
Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val
65                  70                  75                  80
Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln
                85                  90                  95
Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu
            100                 105                 110
Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val
        115                 120                 125
Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro
    130                 135                 140
Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp
145                 150                 155                 160
Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly
                165                 170                 175
Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala
            180                 185                 190
Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe
        195                 200                 205
Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr
    210                 215                 220
Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu
225                 230                 235                 240
Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr
                245                 250                 255
Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile
            260                 265                 270
Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu
        275                 280                 285
Leu Gly Trp Leu
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<210> 33
<211> 316
<212> PRT

<213> Synechocystis sp

<400> 33

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Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg
        35                  40                  45
Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala
    50                  55                  60
Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp
65                  70                  75                  80
Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val
                85                  90                  95
Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser
            100                 105                 110
Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala
        115                 120                 125
Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys
    130                 135                 140
Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile
145                 150                 155                 160
Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr
                165                 170                 175
Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe
            180                 185                 190
Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val
        195                 200                 205
Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile
    210                 215                 220
Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr
225                 230                 235                 240
Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu
                245                 250                 255
Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly
            260                 265                 270
Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu
        275                 280                 285
Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His
    290                 295                 300
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Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly
305 310 315

<210> 34
<211> 324
<212> PRT
<213> Synechocystis sp

<400> 34
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1 5 10 15
Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys
20 25 30
Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp
35 40 45
Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val
50 55 60
Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu
65 70 75 80
Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile
85 90 95
Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser
100 105 110
Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile
115 120 125
Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile
130 135 140
Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser
145 150 155 160
Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala
165 170 175
Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu
180 185 190
Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser
195 200 205
Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu
210 215 220
Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile
225 230 235 240
Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala
245 250 255

Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr
260 265 270
Ile Val Leu Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr
275 280 285
Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala
290 295 300
Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly
305 310 315 320
His Ala Gly Ile

<210> 35
<211> 307
<212> PRT
<213> Synechocystis sp

<400> 35
Met Thr Glu Ser Ser Pro Leu Ala Pro Ser Thr Ala Pro Ala Thr Arg
1 5 10 15
Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val
20 25 30
Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln
35 40 45
Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile
50 55 60
Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly
65 70 75 80
Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg
85 90 95
Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu
100 105 110
Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu
115 120 125
Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro
130 135 140
Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr
145 150 155 160
Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser
165 170 175
Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr
180 185 190

Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu
195 200 205
Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly
210 215 220
Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala
225 230 235 240
Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile
245 250 255
Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr
260 265 270
His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn
275 280 285
Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala
290 295 300
Gly Leu Gly
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<210> 36
<211> 927
<212> DNA
<213> Synechocystis sp

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cctgcttccc tggatttagt gttcggcgct tggctggcct gcctgttggg taatgtgtac 180
attgtcggcc tcaaccaatt gtgggatgtg gacattgacc gcatcaataa gccgaatttg 240
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gttgcttcct tggcgatcgc ctggggatta gggctatggc tggggctaac ggtgggcatt 360
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cggggaacct taatttact cactggttgt tatttagcca tggcaatctg gggcttatgg 720
gcggctatgc ctttaaatac tgctttcttg attgtttccc atttgtgctt attagcctta 780
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<210> 37

<211> 308
<212> PRT
<213> Synechocystis sp

<400> 37

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Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
            20                  25                  30
Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
        35                  40                  45
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
    50                  55                  60
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65                  70                  75                  80
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
                85                  90                  95
Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
            100                 105                 110
Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
        115                 120                 125
Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
    130                 135                 140
Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145                 150                 155                 160
Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
                165                 170                 175
Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
            180                 185                 190
Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
        195                 200                 205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
    210                 215                 220
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225                 230                 235                 240
Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
                245                 250                 255
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
            260                 265                 270
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
        275                 280                 285
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Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
290 295 300
Asn Thr Ile Phe
305

<210> 38
<211> 1092
<212> DNA
<213> Synechocystis sp

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tggtacgtgc gcctgctttt gccccaatcc ggggaaagtt ttgcttttat gtactccatc 120
gaaaatcctg ctagcgatca tcattacggc ggcggtgctg tgcaaatttt agggccggct 180
acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa 240
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aggcaggcga aacccctact ctccgaagaa ttttttgcca cggtcaagga aggttatcaa 360
atccatcaaa atcagcacca aggacaaatc attcatggcg atcgccattg tcgttggcag 420
ttcaccgtag aaccggaagt aacttggggg agtcctaacc gatttcctcg ggctacagcg 480
ggttggcttt ccttttttacc cttgtttgat cccggttggc aaattctttt agcccaaggt 540
agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgacca cgccctagtt 600
tatgccgaaa aaaattgggg tcactccttt ccctcccgct ggttttggct ccaagcaaat 660
tattttcctg accatccagg actgagcgtc actgccgctg gcggggaacg gattgttctt 720
ggtcgccccg aagaggtagc tttaattggc ttacatcacc aaggtaattt ttacgaattt 780
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gtgccattct ga 1092

<210> 39
<211> 363
<212> PRT
<213> Synechocystis sp

<400> 39
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1 5 10 15
Phe Phe Glu Gly Trp Tyr Val Arg Leu Leu Leu Pro Gln Ser Gly Glu
20 25 30

Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His
35 40 45
Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln
50 55 60
Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys
65 70 75 80
Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys
85 90 95
Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe
100 105 110
Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly
115 120 125
Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu
130 135 140
Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala
145 150 155 160
Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu
165 170 175
Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln
180 185 190
Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His
195 200 205
Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp
210 215 220
His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu
225 230 235 240
Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn
245 250 255
Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala
260 265 270
Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val
275 280 285
Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro
290 295 300
Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr
305 310 315 320
Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly
325 330 335
Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr
340 345 350
Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe

355 360

<210> 40
<211> 56
<212> DNA
<213> Artifical Sequence

<400> 40
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<210> 41
<211> 32
<212> DNA
<213> Artifical Sequence

<400> 41
tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 42
<211> 32
<212> DNA
<213> Artifical Sequence

<400> 42
tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 43
<211> 32
<212> DNA
<213> Artifical Sequence

<400> 43
tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 44
<211> 32
<212> DNA
<213> Artifical Sequence

<400> 44
tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 45
<211> 36
<212> DNA
<213> Artifical Sequence

<400> 45
tcgaggatcc gcggccgcaa gcttcctgca ggagct 36

<210> 46
<211> 28
<212> DNA
<213> Artifical Sequence

<400> 46
cctgcaggaa gcttgcggcc gcggatcc 28

<210> 47
<211> 36
<212> DNA
<213> Artifical Sequence

<400> 47
tcgacctgca ggaagcttgc ggccgcggat ccagct 36

<210> 48
<211> 28
<212> DNA
<213> Artifical Sequence

<400> 48
ggatccgcgg ccgcaagctt cctgcagg 28

<210> 49
<211> 39
<212> DNA
<213> Artifical Sequence

<400> 49
gatcacctgc aggaagcttg cggccgcgga tccaatgca 39

<210> 50
<211> 31
<212> DNA
<213> Artifical Sequence

<400> 50
ttggatccgc ggccgcaagc ttcctgcagg t 31

<210> 51
<211> 41
<212> DNA
<213> Artifical Sequence

<400> 51
ggatccgcgg ccgcacaatg gagtctctgc tctctagttc t 41

<210> 52
<211> 38
<212> DNA
<213> Artifical Sequence

<400> 52
ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

<210> 53
<211> 45
<212> DNA
<213> Artifical Sequence

<400> 53
ggatccgcgg ccgcacaatg gcgttttttg ggctctcccg tgttt 45

<210> 54
<211> 40
<212> DNA
<213> Artifical Sequence

<400> 54
ggatcctgca ggttattgaa aacttcttcc aagtacaact 40

<210> 55

<211> 38
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<400> 55
ggatccgcgg ccgcacaatg tggcgaagat ctgttgtt 38

<210> 56
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<400> 56
ggatcctgca ggtcatggag agtagaagga aggagct 37

<210> 57
<211> 50
<212> DNA
<213> Artifical Sequence

<400> 57
ggatccgcgg ccgcacaatg gtacttgccg aggttccaaa gcttgcctct 50

<210> 58
<211> 38
<212> DNA
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<400> 58
ggatcctgca ggtcacttgt ttctggtgat gactctat 38

<210> 59
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<400> 59
ggatccgcgg ccgcacaatg acttcgattc tcaacact 38

<210> 60
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<212> DNA
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<400> 60
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<210> 61
<211> 22
<212> DNA
<213> Artifical Sequence

<400> 61
taatgtgtac attgtcggcc tc 22

<210> 62
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<212> DNA
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<400> 62
gcaatgtaac atcagagatt ttgagacaca acgtggcttt ccacaattcc ccgcaccgtc 60

<210> 63
<211> 22
<212> DNA
<213> Artifical Sequence

<400> 63
aggctaataa gcacaaatgg ga 22

<210> 64
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<400> 64
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggaattgg tttaggttat 60
ccc 63

<210> 65
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<212> DNA
<213> Artifical Sequence

<400> 65
ggatccatgg ttgcccaaac cccatc 26

<210> 66
<211> 61
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<400> 66
gcaatgtaac atcagagatt ttgagacaca acgtggcttt gggtaagcaa caatgaccgg 60
c 61

<210> 67
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<212> DNA
<213> Artifical Sequence

<400> 67
gaattctcaa agccagccca gtaac 25

<210> 68
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<400> 68
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgggtgcga aaagggtttt 60
ccc 63

<210> 69
<211> 23
<212> DNA
<213> Artifical Sequence

<400> 69
ccagtggttt aggctgtgtg gtc 23

<210> 70

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<400> 70
ctgagttgga tgtattggat c 21

<210> 71
<211> 28
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<400> 71
ggatccatgg ttacttcgac aaaaatcc 28

<210> 72
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<212> DNA
<213> Artifical Sequence

<400> 72
gcaatgtaac atcagagatt ttgagacaca acgtggcttt gctaggcaac cgcttagtac 60

<210> 73
<211> 28
<212> DNA
<213> Artifical Sequence

<400> 73
gaattcttaa cccaacagta aagttccc 28

<210> 74
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<400> 74
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<210> 75

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<400> 75
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<400> 76
gtatgcccaa ctggtgcaga gg 22

<210> 77
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<400> 77
ggatccatgt ctgacacaca aaataccg 28

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<400> 78
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ag 62

<210> 79
<211> 27
<212> DNA
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<400> 79
gaattctcaa atccccgcat ggcctag 27

<210> 80

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<400> 80
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<210> 81
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<400> 81
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<210> 82
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<400> 82
gcaatacccg cttggaaaac g 21

<210> 83
<211> 29
<212> DNA
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<400> 83
ggatccatga ccgaatcttc gcccctagc 29

<210> 84
<211> 61
<212> DNA
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<400> 84
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g 61

<210> 85
<211> 27
<212> DNA
<213> Artifical Sequence

<400> 85
gaattcttag cccaggccag cccagcc 27

<210> 86
<211> 66
<212> DNA
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<400> 86
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attacc 66

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<400> 87
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<400> 88
gcagactggc aattatcagt aacg 24

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<400> 89
ccatggattc gagtaaagtt gtcgc 25

<210> 90
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<400> 90
gaattcactt caaaaaaggt aacag

<210> 91
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<400> 91
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cgattaagat taggaaaaat ttataaccgg taattaagaa aacattaacc gtagtaaccg 180
taaatgccga ttcctccctt gtctaaaaga cagaaaacat atattttatt ttgccccata 240
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GGAACTGCTTATTCAATCAATGTGCCTCTGTTGAGATGGAAGAGGTTTGCAGTGCTTGCAGCGATGTGCATTCTAGCT
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<210> 96
<211>
<212> DNA
<213> soy

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<210> 97

<211>

<212> PRT

<213> soy

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LNQLSDVEIDKINKPYLPLASGEYSFETGVTIVASFSILSFWLGWVVGSWPLFWALFVSFVLGTAYSINVPLLRWKRF
AVLAAMCILAVRAVIVQLAFFLHIQTHVYKRPPVFSRSLIFATAFMSFFSVVIALFKDIPDIEGDKVFGIQSFSVRLG
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IPFVR

<210> 98

<211>

<212> PRT

<213> soy

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LEAVVAALFMNIYIVGLNQLSDVEIDKINKPYLPLASGEYSFETGVTIVASFSILSFWLGWVVGSWPLFWALFVSFVL
GTAYSINVPLLRWKRFAVLAAMCILAVRAVIVQLAFFLHMQTHVYKRPPVFSRPLIFATAFMSFFSVVIALFKDIPDI
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<210> 99

<211>

<212> DNA

<213> rice

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GCTCTGGTTTATTGATAGCAAATTATGTTGCTGCTATTGCTGTAGCTTTTCTCATGCCTC
AGGCTTTCAGGCGCACTGTAATGGTGCCTGTGCATGCTGCCCTTGCCGTTGGTATAATTT
TCCAGACATGGGTTCTGGAGCAAGCAAAATATACTAAGGATGCTATTTCACAGTACTACC
GGTTCATTTGGAATCTCTTCTATGCTGAATACATCTTCTTCCCGTTGATATAGAGACCAA
GCAATCTGATATGGTCTGCATGTTGAGTGCGGCAAAAACTAGAAGCCCATATGAACAGTG
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CTGTAAAGGGTAAGCACTGTTGGGCATATATATGAAAGGAAGGTGATAAAGCAGGGATGC
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AAAAACGACCTTGTTTTACACTACCAAGGGAGGTTAACTCTAGTTTTCATGTGACCACTT
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<210> 100

<211>

<212> DNA

<213> wheat

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TTTTCTCCACATTCAGACATTTGTTTTCAGAAGGCCGGCAGACTTTTCAAAGCCATTGAT
ATTTGCAACTGCCTTCATGACATTCTTCTCAGTTGTAATAGCATTATTCAAGGATATACC
CGATATTGAAGGGGACCGCATCTTTGGAATCCAATCTTTTAGTGGTAGACTAGGTCAAAG
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C

<210> 101
<211>
<212> DNA
<213> leek

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CCCAAGAATTGCATGACCTATCACTGTTAAGCATTTGCTCCATAGGCATGAGGAAGTAGC
TCCAACAACCATGACAACAGTGTAGGCCATCTCAAGGAGATATATACATATCCAAAACAC
CCTCTCCTGGCCAAGGCGCACGCTGAAAGAATGGATGCCAAATATTTTGTCTCCGTCTAT
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<210> 102
<211>
<212> DNA
<213> leek

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CATGTGAAACCAAGGTTTACAACATGTAGTAGGTCTCAAAAACTTGGTCATGTAAAAGCC
ACATCCGAGCATTCTTTAGAATCTGGATCCGAAGGATACACTCCTAGAAGCATATGGGAA
GCCGTACTAGCTTCACTGAATGTTCTATACAAATTTTCACGACCTCACACAATAATAGGA
ACAGCAATGGGCATAATGTCAGTTTCTTTGCTTGTTGTCGAGAGCCTATCCGATATTTCT
CCTCTGTTTTTTGTGGGATTATTAGAGGCTGTGGTTGCTGCATTGTTTATGAATGTTTAC
ATTGTAGGTCTGAATCAATTATTTGACATAGAAATAGACAAGGTCAATAAACCTGATCTT
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<210> 103
<211>
<212> DNA
<213> canola

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TATTTGGAACTTGCGATCTCCTTCAACATCAGGAAGATCTTTTGTAATAGCAATGACTAG
TGCAAACAGTGTCACAAAAGACGTGATGAAAGCCACAGGTGCACTCCACTGAAACGAAAG

TCCAAGAGCAGCTCTAGTAGCATGGTACACACCAAAATTAAGAAGAAAACCTCGTACCGT
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<210> 104

<211>

<212> DNA

<213> corn

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GAAATGGTGAAGGACGAATTTGCTTTTCTAGCCAAAGGACCCAAGGTCCTACCTTGCATC
ACCATCAGAAATTCTTCGAATGGAAATCCTCCTATTGTAGGATATCACATCGGTCATTAA
ATACTTCTGTTAATGCTTCGGGGCAACAGCTGCAGTCTGAACCTGAAACACATGATTCTA
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TGCTCATCCCTCTGGTGCGGTGAGCGCGAGGCGAGGTGGTGGCAGACGGATCGGCGTCGG
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<210> 105

<211>

<212> DNA

<213> corn

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CCGTGCGGCCCGGCGCGGCCCGCCCGCGAGATCATTTTCTACCACCATGTTGTTCCATAC
AACGAAATGGTGAAGGACGAATTTGCTTTTCTAGCCAAAGGACCCAAGGTCCTACCTTGC
ATCACCATCAGAAATTCTTCGAATGGAAATCCTCCTATTGTAGGATATCACATCGGTCAT
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<210> 106

<211>

<212> DNA

<213> corn

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GATGGACGCGCTTCGCCTACGGCCGTCCCTCCTCCCCGTGCGGCCCGGCGCGGCCCGCCC
GCGAGGCAGTGGTAGCTGCCCTTTTCATGAATATCTATATTGTTGGACTGAACCAGTTAT
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CCCTTGCAACTGGGGTTGCAATAGTTTCGGTCTTTGCCGCTATGAGCTTTGGCCTTGGAT
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CATATTCAATCAATCTGCCGTACCTTCGATGGAAGAGATTTGCTGTTGTTGCAGCACTGT
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<210> 107

<211>

<212> DNA

<213> cotton

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TGCATTTCTTGGTTCCGGACTTCTACTGGTGAATTATGTTGCTGCTGTGTTGGCTGCAAT
ATACATGCCTCAGGCTTTCAGGCGTAGTTTAATGATACCTGCTCATATCTTTTTGGCGGT
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<210> 108

<211>

<212> DNA

<213> tomato

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TGCTGATAAAAAACTTAAAGGGAGATTTTTGGTGCACGCATCATCTGAACACCCTCTTGA
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<210> 109

<211>
<212> DNA
<213> *Arabidopsis*

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TGTATCTCCTCTCACTCGCTCACTAGTTCCGTTCCGATCGACTAAACTAGTTCCCCGCTC
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TAAACCTGTTTACGTCCCGACGTCTCCCAATCGCGAACTCCGGACTCCTCACAGTGGATA
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AGAGAAGAGGGAGAGTTTTTGTTTTATGTATTCTGTGGAGAATCCTGCATTTCGGCAGAG
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TCCATTTTGGCATCAAGGTCACATTTGCGATGATGGCCGTACTGACTATGCGGAAACTGT
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CTTCAAGCCACCGGGTCTGTAACATTGATGAGTGTTTTGTTTGTTGATAGAGACCCATGT
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<210> 110
<211>
<212> PRT
<213> *Arabidopsis*

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IPEKRESFCFMYSVENPAFRQSLSPLEVALYGPRFTGVGAQILGANDKYL
CQYEQDSHNFWGDRHELVLGNTFSAVPGAKAPNKEVPPEEFNRRVSEGFQ
ATPFWHQGHICDDGRTDYAETVKSARWEYSTRPVYGWGDVGAKQKSTAGW
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KWFWVQCNVFEGATGEVALTAGGGLRQLPGLTETYENAALVCVHYDGKMY
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GLATACRDSCYGELKLQIWERLYDGSKGKVILETKSSMAAVEIGGGPWFG
TWKGDTSNTPELLKQALQVPLDLESALGLVPFFKPPGL*